



SEQUENCE LISTING

<110> Kazuhiro MACHIDA et al.

<120> DNA PARTICIPATING IN HYDROXYLATION OF MACROLIDE COMPOUND

<130> 0425-1257PUS1

<140> US 10/577,655

<141> 2006-05-01

<150> JP 2003-396828

<151> 2003-11-27

<160> 19

<210> 1

<211> 3793

<212> DNA

<213> Streptomyces sp.

<220>

<221> CDS

<222> (1322)..(2548)

<220>

<221> CDS

<222> (2564)..(2761)

<400> 1

ctgcagctcg	acgtgcgggt	cggacttcac	gttgaagtac	cagaccggat	gcttgggcgc	60
accgcccagc	gaggcgaccg	ccgcgtaact	cccctcgtgc	tcgaccgcga	tcagcggcgt	120
cttgccggtc	tttccgctgc	gcgcgccccg	ggtggtgagc	acgatgaccg	gcagcccggg	180
gtcccgcagc	gtggtgccct	tggtgcccc	ggaactctcg	tacagctcga	cctgctcgcg	240
cacccactgc	gtcgggctgg	gtcgtactc	gccctcaagt	ggcaagggat	ccgtctcctt	300
cgtcgggtccg	gcggatgggt	ctccggacgg	tcccaactcc	cgcgcccgcc	cggatcatcc	360
gtaccgcatg	ccccttcgcc	cgagcgggtg	atcaccgttc	cggccatccg	gtcgtccgca	420
ccgcgagcac	caggatcacg	gcgctggaga	gcaggggcgt	gaccagccgc	ccccgggtggc	480
ccgtcagggc	gcgaccagc	agcgcgcccc	cgcccgccag	cagtagctgc	cagctcgcgg	540
acgcggcgaa	ggccgcccgc	gcgaacaccg	cccgtttcag	cggccgtgcc	gcaccggcgg	600
cgccgctgcc	gagcaccagc	gccacgaagt	agaccaccgt	catgggattg	agcagggtga	660
tcccagagaag	gccgagataa	gcccctgccg	cgccctggaac	cggccgttcc	gggcgggtgg	720
tgagccgatg	ggcgcggtac	tgccgcaggg	cgagcagcgc	cgcccgcagc	gcgagcaccg	780
cgaggaccag	cgccgaggcc	cagcgcagcg	ggtccagcac	cggccgcagc	tgtgccgcga	840
gggcggcgcc	gcccacggtc	gcgagcagcg	cgtacagccc	gtcggccgtg	gcgacgccga	900
gcgcccgcga	ggcgccgggt	cgagcgagg	tgcgggcggg	gagggagacc	agataggtcc	960
cgaccgcgcc	gacgggcacc	gcgatgccgt	acccggcgag	caggcccgcg	agcagcgcg	1020
ccgtcacggg	cgtgcgggac	tggttcctcc	ggggacggcg	gggctgctgt	cggcccggca	1080
ccgcggggcg	ggtggcagcg	ggcgtcggca	ggaggaggc	tgtaggaggc	atgggccgat	1140
cctggggccg	ccgcgcccgc	accggcaa	gaattacggc	gcgttcagc	ccccggccgg	1200
ctcgtctctt	ggccacttca	ccgcgtacgg	cgatctggcc	gaacttgctg	tcgcccata	1260
ggtgcctcgg	gcattctaat	aagatcgcca	cgacgcacct	cttcgtctgc	gaggtctttc	1320
c atg acg gaa ctg acg gac atc acc ggc ccg ggg acc ccg gcc gaa						1366
Met Thr Glu Leu Thr Asp Ile Thr Gly Pro Gly Thr Pro Ala Glu						
1	5	10	15			
ccc gtc gca ttc ccc cag gac cgc acc tgc ccc tac cac ccc ccc acc						1414
Pro Val Ala Phe Pro Gln Asp Arg Thr Cys Pro Tyr His Pro Pro Thr						

				20					25				30				
gga	tac	ggc	ccg	ctg	cgc	gac	ggg	cgc	agc	ctg	tcc	cgc	gtc	acc	ctc		1462
Gly	Tyr	Gly	Pro	Leu	Arg	Asp	Gly	Arg	Ser	Leu	Ser	Arg	Val	Thr	Leu		
			35					40				45					
ttc	gac	ggc	cgc	gag	gtc	tgg	atg	gtc	acg	ggc	cac	gcc	acc	gcc	cgc		1510
Phe	Asp	Gly	Arg	Glu	Val	Trp	Met	Val	Thr	Gly	His	Ala	Thr	Ala	Arg		
		50					55				60						
gcg	ctg	ctc	gcg	gac	ccc	cgg	ctg	tcc	acc	gac	cgc	acc	ctc	ccg	ggc		1558
Ala	Leu	Leu	Ala	Asp	Pro	Arg	Leu	Ser	Thr	Asp	Arg	Thr	Leu	Pro	Gly		
	65					70			75								
ttc	ccc	gtg	ccc	acg	gcc	cgc	ttc	gcg	gcc	gtc	cgc	gac	cgg	cgg	gtg		1606
Phe	Pro	Val	Pro	Thr	Ala	Arg	Phe	Ala	Ala	Val	Arg	Asp	Arg	Arg	Val		
	80					85				90					95		
gcg	ctg	ctc	ggc	gtg	gac	gac	ccg	gtc	cac	cag	acc	cag	cgg	cgg	atg		1654
Ala	Leu	Leu	Gly	Val	Asp	Asp	Pro	Val	His	Gln	Thr	Gln	Arg	Arg	Met		
			100					105						110			
atg	atc	ccg	tcg	ttc	acc	ctc	aag	cgc	gcg	gcc	ggg	ctg	cgg	ccc	acc		1702
Met	Ile	Pro	Ser	Phe	Thr	Leu	Lys	Arg	Ala	Ala	Gly	Leu	Arg	Pro	Thr		
			115					120					125				
atc	cag	cgg	acc	gtc	gac	ggg	ctg	ctg	gac	gcg	atg	atc	gag	aag	ggg		1750
Ile	Gln	Arg	Thr	Val	Asp	Gly	Leu	Leu	Asp	Ala	Met	Ile	Glu	Lys	Gly		
		130				135					140						
ccg	ccg	gcc	gag	ctg	gtc	tcc	gcc	ttc	gcc	ctg	ccc	gtg	ccc	tcg	gtg		1798
Pro	Pro	Ala	Glu	Leu	Val	Ser	Ala	Phe	Ala	Leu	Pro	Val	Pro	Ser	Val		
	145					150					155						
gtc	atc	tgc	ggc	ctg	ctc	ggc	gtg	ccg	tac	gcc	gac	cac	gag	ttc	ttc		1846
Val	Ile	Cys	Gly	Leu	Leu	Gly	Val	Pro	Tyr	Ala	Asp	His	Glu	Phe	Phe		
	160					165				170					175		
gag	gaa	cag	tcc	cgc	acg	ctg	ctg	cgc	ggt	ccc	acg	gcc	gcc	gac	tcg		1894
Glu	Glu	Gln	Ser	Arg	Thr	Leu	Leu	Arg	Gly	Pro	Thr	Ala	Ala	Asp	Ser		
			180					185						190			
caa	ggg	gcg	cgc	gag	cgg	ctc	gag	gag	tac	ctc	ggc	ggg	ctg	atc	gac		1942
Gln	Gly	Ala	Arg	Glu	Arg	Leu	Glu	Glu	Tyr	Leu	Gly	Gly	Leu	Ile	Asp		
			195				200						205				
gac	aag	gag	cgg	cag	gcc	gaa	ccc	ggc	gac	ggc	gtc	ctg	gac	gac	ctc		1990
Asp	Lys	Glu	Arg	Gln	Ala	Glu	Pro	Gly	Asp	Gly	Val	Leu	Asp	Asp	Leu		
	210					215						220					
gtc	cac	cag	cgg	ctg	cgc	acc	ggc	gag	ctg	gac	cgg	cgc	gac	gtg	gtg		2038
Val	His	Gln	Arg	Leu	Arg	Thr	Gly	Glu	Leu	Asp	Arg	Arg	Asp	Val	Val		
	225					230					235						
gcg	ctg	gcc	gtc	atc	ctg	ctc	gtg	gcc	ggg	cac	gag	acg	acc	gcc	aac		2086
Ala	Leu	Ala	Val	Ile	Leu	Leu	Val	Ala	Gly	His	Glu	Thr	Thr	Ala	Asn		
	240				245				250						255		
atg	atc	tcc	ctc	ggc	acc	tac	acg	ctg	ctg	cgg	cac	ccc	ggc	cgg	ctg		2134
Met	Ile	Ser	Leu	Gly	Thr	Tyr	Thr	Leu	Leu	Arg	His	Pro	Gly	Arg	Leu		
			260					265						270			
gcc	gag	ctg	cgc	gcc	gac	ccg	gcg	ctg	ctg	ccc	gcc	gcc	gtg	gag	gag		2182
Ala	Glu	Leu	Arg	Ala	Asp	Pro	Ala	Leu	Leu	Pro	Ala	Ala	Val	Glu	Glu		
		275					280						285				
ctg	atg	cgg	atg	ctc	tcg	atc	gcg	gac	ggg	ctg	ctg	cgc	ctg	gcc	ctg		2230
Leu	Met	Arg	Met	Leu	Ser	Ile	Ala	Asp	Gly	Leu	Leu	Arg	Leu	Ala	Leu		
		290					295					300					
gag	gac	atc	gag	atc	gcc	ggc	gcc	acg	atc	cgg	gcc	ggc	gag	ggc	gtc		2278
Glu	Asp	Ile	Glu	Ile	Ala	Gly	Ala	Thr	Ile	Arg	Ala	Gly	Glu	Gly	Val		
	305					310					315						
ctg	ttc	tcc	acc	tcg	ctg	atc	aac	cgc	gac	gag	tcc	gtg	ttc	gac	gac		2326
Leu	Phe	Ser	Thr	Ser	Leu	Ile	Asn	Arg	Asp	Glu	Ser	Val	Phe	Asp	Asp		

320	325	330	335	
ccc gac acc ctg gac ttc cac cgc tcc acc cgc cac cac gtg gcc ttc				2374
Pro Asp Thr Leu Asp Phe His Arg Ser Thr Arg His His Val Ala Phe				
	340	345	350	
ggt ttc ggc atc cac cag tgc ctg ggc cag aac ctg gcc cgc gcc gag				2422
Gly Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala Glu				
	355	360	365	
ctg gag atc gcc ctg ggc acg ctc ctg gag cgg ctc ccc ggc ctc cgg				2470
Leu Glu Ile Ala Leu Gly Thr Leu Leu Glu Arg Leu Pro Gly Leu Arg				
	370	375	380	
ctg gcc gcg ccc gcc gag gag atc ccg ttc aaa ccc ggc gac acg atc				2518
Leu Ala Ala Pro Ala Glu Glu Ile Pro Phe Lys Pro Gly Asp Thr Ile				
	385	390	395	
cag ggg atg ctg gaa ctc ccc gtg acc tgg taa gaggctctgg tc atg cac				2569
Gln Gly Met Leu Glu Leu Pro Val Thr Trp			Met His	
	400	405	410	
atc gac atc gac aag gac cgc tgc atc ggc gcc ggc cag tgc gcg ctg				2617
Ile Asp Ile Asp Lys Asp Arg Cys Ile Gly Ala Gly Gln Cys Ala Leu				
	415	420	425	
gcc gcc ccg ggc gtg ttc acc cag gac gac gac ggc tac agc acc ctg				2665
Ala Ala Pro Gly Val Phe Thr Gln Asp Asp Asp Gly Tyr Ser Thr Leu				
	430	435	440	
ctc ccc ggc cgc gag gac ggc ggg ggc gac ccg atg gtc cgg gag gcg				2713
Leu Pro Gly Arg Glu Asp Gly Gly Gly Asp Pro Met Val Arg Glu Ala				
	445	450	455	
gcc cgc gcc tgc ccg gtg agc gcc atc ccg gtg acc gaa ccg gcc ggc				2761
Ala Arg Ala Cys Pro Val Ser Ala Ile Arg Val Thr Glu Pro Ala Gly				
	460	465	470	475
tga ggcggggccc ggcggccgcg gcccgtgcc gggaccgcg ttcccagttc agtagg				2820

gtcgtgcat	gacctcacag	gccgggaagc	ccttccctcta	cgtcgtcgtc	tgcgcggccg	2880
ggaccgccgc	cggagtcacc	acgtgatcg	gcgcgcgcca	ggcgcggggc	tgggaggtgg	2940
gggtccctggc	cacgccggtg	gcgatgggcg	ggttcttcga	cacggctgcg	gtcgaggaga	3000
tgacggggccg	gcccatecgc	tcggcctggc	gctcgccggc	cgatccgcgc	ccgttcccgc	3060
cgccggggcgc	cgtggtggtg	gcgcccgcc	ccttcaacac	cgtcaacaag	tgggcggccg	3120
gtctcgccga	cacgctcgcc	gtcggcacgc	tctgcgaggc	ggcgggcctc	ggcgtgccga	3180
tcgccgtcct	gccctgctg	gcggacgcgc	tggccgcccc	ccccgcgtac	cgggagggcc	3240
ttctccggct	gcgtgggatg	ggcgtccgct	tcggcgagcc	gtacgccggc	ccgccggggg	3300
aggacggcga	ggcggacggc	gcacggcccc	ggttcgcctg	ggagaacgcc	ctggacctgc	3360
tggagcgggc	ctgaaccgcg	tccccgaccc	gtagggcctg	tctgacactg	tcagacaggc	3420
cctaacggca	ggtcagcgcc	ggcccggcca	gcatgccgcc	ggtgtagagg	tcctggcccc	3480
gcggcagcca	gtagcccagc	ctggagacca	ccgtggagca	gtcaggcccc	acggtgacgc	3540
ggaccttcac	cgtctcggga	cggccgggct	gcagcgcggt	cagcgcgcag	tccagggagt	3600
acgcgagccg	ggtcttcgag	gtaccggccg	accagcgggt	tgacgcagcg	ggcgtcgtcc	3660
gtggcgatcc	gcaccccggg	gcccgcgccg	ccgatgagtc	cgagccgggc	gctgccgtcg	3720
ccctcgtcgc	tgtcccggcg	gaccgtgtag	gtcagcgtgg	tgggtggcgtc	gcgccgcagg	3780
gtgtccggtc	gac					3793

<210> 2
 <211> 2329
 <212> DNA
 <213> Streptomyces sp.

<220>
 <221> CDS

<222> (420)..(1604)

<220>

<221> CDS

<222> (1643)..(1834)

<400> 2

```
ggatccacggtgtggccgcccgcctcgccccgggtgaccgaccggcggtatcggtctatgtcgc60
cgcgctcttcgcggcgctgggcttccccgagggcgaggcgcgggaccgcgccctgctggc120
gtacaccgccctacctcggccacaccagctcggacatgccgtccgacagagcctgccggc180
cgaggcgccaacgaccgctatctggatggcgtgatcgacaccctcgtaggcccgcggga240
cgaggcgcatgaagccgaacatgtcaccaatctgaacgaggttggcggaactgcgcgcaga300
acatgcccggtatccgcggcctatgaggtgagatcggcgcggcgaaacacggtgcgccacag360
cgttgccatctcacacacgagcaactcgagccacttgagctcgtacgggaggaaattc419

gtgaccgaagccatccctactttcagaaacgcaccgtgtcccactcac467
ValThrGluAlaIleProTyrPheGlnAsnArgThrCysProTyrHis
15
ccgcccgccgccctatcagccactgcgcggggccggcccgctgagccat515
ProProAlaAlaTyrGlnProLeuArgGlyAlaGlyProLeuSerHis
202530
gtcacgttctactacggcggaaggtgttggtgcgtcaccggccacccc563
ValThrPheTyrAspGlyArgLysValTrpAlaValThrGlyHisPro
354045
gaggcagcggtgctgctgaccgacgagcagcgactctccgccgaccgag611
GluAlaArgAlaLeuLeuThrAspGlnArgLeuSerAlaAspArgGln
505560
aacccggccctccggtcctcttcgaacgcttcggtccatccgcgcg659
AsnProAlaPheProValProPheGluArgPheAlaAlaIleArgArg
65707580
gtccggaacccgtgatccggcgaccgagcacaaaccag707
ValArgThrProLeuIleGlyValAspAspProGluHisAsnThrGln
859095
cgccggaatctatccagccttcagctcaagcggaccgccgcactg755
ArgArgMetLeuIleProSerPheSerLeuLysArgThrAlaAlaLeu
100105110
cgcccgagatccagcggatcgtcgacgggctgctcgaccggatgctg803
ArgProGluIleGlnArgIleValAspGlyLeuLeuAspArgMetLeu
115120125
gatcaggcccgcccaccgagctgctctccggttcgccctgcccgtc851
AspGlnGlyProProThrGluLeuValSerAlaPheAlaLeuProVal
130135140
ccgtcgatgtgatctgcgcactgctcggaatctatgccgaccat899
ProSerMetValIleCysAlaLeuLeuGlyValSerTyrAlaAspHis
145150155160
gagttcttcgaggaggtctccgcccgcacatcgggccgtcgccc947
GluPhePheGluGluGluSerArgArgIleLeuArgGlyArgSerAla
165170175
gaggaggcggaggaccgcccggtgaaatgaggagtacttaccggg995
GluGluAlaGluAspAlaArgLeuLysLeuGluGluTyrPheThrGly
180185190
ctgatccgccgaagaggaagaacccggggacgggctgctgacgag1043
LeuIleAlaAlaLysGluLysAsnProGlyAspGlyLeuLeuAspGlu
195200205
ctgatcgaggaccggtgaccggaccggcgctcaccgcgacgagctg1091
LeuIleGluAspArgLeuArgThrGlyAlaLeuThrArgAspGluLeu
210215220
```

gtc cgg ctc gcc atg atc ctg ctg gtg gcc ggc cat gag acc acc gcc	1139
Val Arg Leu Ala Met Ile Leu Leu Val Ala Gly His Glu Thr Thr Ala	
225 230 235 240	
aac atg atc tcg ctc ggc acc ttc acc ctg ctg gag cac ccc gag cag	1187
Asn Met Ile Ser Leu Gly Thr Phe Thr Leu Leu Asp His Pro Glu Gln	
245 250 255	
ctg gcg cag ctc aag gcc gac gag ggc ctg atg ccg gcc gcc atc gag	1235
Leu Ala Gln Leu Lys Ala Asp Glu Gly Leu Met Pro Ala Ala Ile Glu	
260 265 270	
gag ctg ctg cga ttc ctg tcc atc gcg gac ggc ctg ctg ccg gtg gcg	1283
Glu Leu Leu Arg Phe Leu Ser Ile Ala Asp Gly Leu Leu Arg Val Ala	
275 280 285	
acg gag gac atc gag atc ggc ggt cag gtg atc ccg gcc gac gac gcg	1331
Thr Glu Asp Ile Glu Ile Gly Gly Gln Val Ile Arg Ala Asp Asp Ala	
290 295 300	
gtc ctg ttc ccc gcc tca ctg atc aac ccg gac gag gcc gcc tat ccg	1379
Val Leu Phe Pro Ala Ser Leu Ile Asn Arg Asp Glu Ala Ala Tyr Pro	
305 310 315 320	
gca ccc gac gag ctg gac ctc ggc cgt tcg gcc cgc cat cac gtg gcg	1427
Ala Pro Asp Glu Leu Asp Leu Gly Arg Ser Ala Arg His His Val Ala	
325 330 335	
tcc ggc ttc ggg atc cac cag tgc ctg ggg cag aac ctc gcc cgc gcg	1475
Ser Gly Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala	
340 345 350	
gag atg gag atc gcg ctg cgc tca ctg ttc acc agg atc ccg cag ctg	1523
Glu Met Glu Ile Ala Leu Arg Ser Leu Phe Thr Arg Ile Pro Gln Leu	
355 360 365	
cgg ctc gcc gtg ccg gcc gcc gag att ccg ttc aag gac gga gac acc	1571
Arg Leu Ala Val Pro Ala Ala Glu Ile Pro Phe Lys Asp Gly Asp Thr	
370 375 380	
ctg caa ggc atg atc gaa ctg ccg ctg gcc tgg tag cagccaggac ggcaga	1623
Leu Gln Gly Met Ile Glu Leu Pro Leu Ala Trp	
385 390 395	
ccaaagaaag ggggtccgga atg ccg atc gcg atc gac acc gac cgc tgt atc	1675
Met Arg Ile Ala Ile Asp Thr Asp Arg Cys Ile	
400 405	
ggc gcc ggc cag tgt gcc ctg acc gcg ccc ggg ggt ttc acc cag gat	1723
Gly Ala Gly Gln Cys Ala Leu Thr Ala Pro Gly Gly Phe Thr Gln Asp	
410 415 420	
gac gac ggt ttc agt gca ctg ctg ccc ggc ccg gag gac ggc gcc gcc	1771
Asp Asp Gly Phe Ser Ala Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly	
425 430 435	
gac ccg ctg gtg ccg gaa gcc gcc cgc gcc tgc ccc gtg cag gcc att	1819
Asp Pro Leu Val Arg Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile	
440 445 450	
gcg gtc acc gac gat tag cagcaccccc gcggacgacc ccgcagacgc gcgcggcc	1875
Ala Val Thr Asp Asp	
455	
ccggctgaca cccggcgccc gaggcgcgcc cgagccgtcc gccctccac ttgtccctac	1935
ggcatccacc ccatccgcta ccgcaacacc ccttggtga cgggcagttt cgaggacccc	1995
ggtgtgcccg gggcgtagtg gtgaccgtca ccggcttcac gccgcgattg cccacatagg	2055
cgtcgtcgct cgcggcgatc acgaagcgcg gtcggtgcc cggctcgtaa cgggtgcacga	2115
tgccccggcag ttccacggtg aaccgcccgg ccacatcggg caccggggcc ggggccacca	2175
acagggtgcac cagcgtcttc ctgccgttcg gcgcgacatc gtagagcttg gcgaacagca	2235
ccagcttgtc cgcgcgatcc gcggaccgct gcgcccgcgc gccctgcggc gaggcaacct	2295
tcagcgtcac cctcggcgcg cccaccacgt cgac	2329

<210> 3
 <211> 1860
 <212> DNA
 <213> Unknown

 <220>
 <223> Description of Unknown Sequence: nucleotide sequence with coding region
 derived from an unknown source

<220>
 <221> CDS
 <222> (172)..(1383)

<220>
 <221> CDS
 <222> (1399)..(1593)

<400> 3
 cggggatcgt acgccgtacc gtttcggggc aaccgaatta cgatgcggaa tggatggttc 60

 ccagccagat cccgcaggta gccgatctgg ccgaacttga tgtcgtgcac tggatgcctc 120

 gggcatctaa tgaagatcgg cacgacgcat ccttcgtctg cgaggtctcc c atg aca 177
 Met Thr
 1

 gac acg aca gac ctg acc gag ctg tca gat ccc gtc tcc ttc ccc cag 225
 Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe Pro Gln
 5 10 15

 gac cgg agc tgc ccc tac cac ccg ccc acc ggg tac gac ccg ctg cgc 273
 Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro Leu Arg
 20 25 30

 acc gaa cgg ccg ccc gcc cgc atc cgg ctc tac gac ggc cgc ccc gcc 321
 Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg Pro Ala
 35 40 45 50

 tgg ctc gtc acc ggc cac gcc gtc gcc cgt gac ctg ctg gtc gac ccc 369
 Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val Asp Pro
 55 60 65

 cgc ctg tcc acg gac cgc acc cgc tcg ggc ttc ccg gcc aca act ccc 417
 Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr Thr Pro
 70 75 80

 cgc ttc gcc gcg gtc cgc gac cgc aag ccg gcg ctc ctc ggc gtc gac 465
 Arg Phe Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly Val Asp
 85 90 95

 gac ccc aag cac cgc acc cag cgg tgg atg atg atc ccg agc ttc acc 513
 Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser Phe Thr
 100 105 110

 ctc agg cgc gcc acc gag ctc agg ccg cgc atc cag gag atc gtc gac 561
 Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile Val Asp

115	120	125	130	
gaa ctg ctg gac gtg atg atc gcc cag gga ccc ccg gcc gac ctg gtg Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp Leu Val 135 140 145				609
cgt tcc ttc gcg ctg ccg gtg ccg tcc atg gtg atc tgc gcc ctg ctc Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala Leu Leu 150 155 160				657
ggc gtg ccc tac gcc gac cac gag ttc ttc gag gac cag tcc agg cgg Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser Arg Arg 165 170 175				705
ctg ctg cgc gga ccg gcg gcc gag gac acg cag gac gcc cgg gac cgg Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg Asp Arg 180 185 190				753
ctc gcc gcg tac ctg gag gac ctg atc gac gag aag cgg cgc cgg ccc Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg Arg Pro 195 200 205 210				801
ggc gac ggc ctg ctg gac gaa ctc gtc cag cag cgt ctg aac gaa ggc Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn Glu Gly 215 220 225				849
gag ctc gac cgg gag gaa ctg acc gcg ctg gcg atg atc ctg ctg gtc Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu Leu Val 230 235 240				897
gcg ggc cac gag acc acc gcc aac atg atc tcc ctg ggc acc tac acg Ala Gly His Glu Thr Thr Ala Asn Met Ile Ser Leu Gly Thr Tyr Thr 245 250 255				945
ctc ctg ctg cac ccc gaa cgg ctg acc gag ctg cgc gcc gac ccc gcg Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp Pro Ala 260 265 270				993
ctg ctg ccg gcc gcc gtc gag gaa ctg atg cgg atg ctg tcc atc gcg Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser Ile Ala 275 280 285 290				1041
gac gga ctg ctg cgg cag gcc acc gag gac atc gag atc gcc ggg acc Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala Gly Thr 295 300 305				1089
acc atc agg gcc ggg gac ggc gtg gtc ttc tcc acc tct gtc atc aac Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val Ile Asn 310 315 320				1137
cgc gac gag gac gtc tac ccg gcc ccc gag acc ctc gac ttc cac cgc Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe His Arg 325 330 335				1185
tcg acc cgc cac cac gtc gcc ttc ggt ttc gga atc cac cag tgc ctc Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln Cys Leu 340 345 350				1233

ggc cag aac ctc gcc cgc acc gaa ctg gag atc gcc ctg cgc acg ctc Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg Thr Leu 355 360 365 370	1281
ctc gaa cgg ctg ccc acg ctc cgg ctc gcc gcc cca ccg gag gaa atc Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu Glu Ile 375 380 385	1329
ccc ttc aaa ccc ggc gac acc atc cag ggg atg ctg gaa ctc ccc gtc Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu Pro Val 390 395 400	1377
agc tgg taagaggctg ccgtc atg cat atc gag atc gac aag gac cgc tgc Ser Trp Met His Ile Glu Ile Asp Lys Asp Arg Cys 405 410	1428
atc ggc gcc gga cag tgc gcc ctg acc gcc ccg ggt gtg ttc acc cag Ile Gly Ala Gly Gln Cys Ala Leu Thr Ala Pro Gly Val Phe Thr Gln 415 420 425 430	1476
gac gac gac ggc ttc agt gac ctg ttg ccc ggc cgg gag gac ggc gcc Asp Asp Asp Gly Phe Ser Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala 435 440 445	1524
ggc gac ccg atg gtc cgg gag gcc gcc agg gcc tgc ccc gtg agt gcc Gly Asp Pro Met Val Arg Glu Ala Ala Arg Ala Cys Pro Val Ser Ala 450 455 460	1572
atc acg ctg tcc gag gac ggg tagggggccg agccgcgccg cccgccggtc Ile Thr Leu Ser Glu Asp Gly 465	1623
cgctgccgcg gcgccgtgcc gacgcggcgg ccggccggcc cgtccggtgc ccgtcgcgtc	1683
gccccgtggc cccggcggcg gctgattgac taggggtccc gggtagcgca acaggcccag	1743
aagccctccg gggcgccgcc cgcgaaagac accgggacgg cgcccgggaa accccttcct	1803
ctacgtcgtc gtctgcgccg ccggcatcgc cgaaggcgtc agcaagctga tcaccgc	1860

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5Dm-3F Primer

<400> 4
 ttgcsetsc csgtcccstc satggttsat 29

<210> 5
 <211> 21
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence : 5Dm-3R Primer
 <400> 5
 gttgatsays gasgtsgaga a 21
 <210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence : 6PIN-2F Primer
 <400> 6
 gctgcgcctg gccctggagg acatcgagat 30
 <210> 7
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence : 6PIN-2R Primer
 <400> 7
 ctggttcctcg aagaactcgt ggtcggcgta 30
 <210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence : DM-NdeF Primer
 <400> 8
 gcccccatat gacggaactg acggacatca 30
 <210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence : DM-SpeR Primer
 <400> 9
 gggccactag tcagccggcc gggttcggtca 30

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : DM-BglF Primer

 <400> 10
 cgcatagatc ttcacccgag cgggtgatca 30

 <210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : DM-BglR Primer

 <400> 11
 tcccagatc ttgaagggtcc gcgtcaccgt 30

 <210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : 5D-1R Primer

 <400> 12
 aggtgcccag cgagatcatg tt 22

 <210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : 7PIN-2F Primer

 <400> 13
 ccatgaccta gctggtggcc ggccatgaga 30

 <210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : 07-NdeF Primer

 <400> 14

gccccatatg accgaagcca tcccctactt 30

<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 07-SpeR Primer

<400> 15
 gccactagtg ctaatcgtcg gtgaccgcaa 30

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5Dm-2R Primer

<400> 16
 ctggatsgtg tcscscsggyt t 21

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5PIN-2F Primer

<400> 17
 cggaatccac cagtgcctcg gccagaacct 30

<210> 18
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : tpm-NdeF Primer

<400> 18
 ggccccatat gacagacacg acagacctga 30

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : tpm-SpeR Primer

<400> 19

gcgcgactag tccccctacc cgtcctcgga

30